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NEWS 2 "Ask CAS" for self-help around the clock
NEWS 3 DEC 21 IPC search and display fields enhanced in CA/CAplus with the
IPC reform
NEWS 4 DEC 23 New IPC8 SEARCH, DISPLAY, and SELECT fields in USPATFULL/
USPAT2
NEWS 5 JAN 13 IPC 8 searching in IFIPAT, IFIUIDB, and IFICDB
NEWS 6 JAN 13 New IPC 8 SEARCH, DISPLAY, and SELECT enhancements added to
INPADOC
NEWS 7 JAN 17 Pre-1988 INPI data added to MARPAT
NEWS 8 JAN 17 IPC 8 in the WPI family of databases including WPIFV
NEWS 9 JAN 30 Saved answer limit increased
NEWS 10 JAN 31 Monthly current-awareness alert (SDI) frequency
added to TULSA
NEWS 11 FEB 21 STN AnaVist, Version 1.1, lets you share your STN AnaVist
visualization results
NEWS 12 FEB 22 Status of current WO (PCT) information on STN
NEWS 13 FEB 22 The IPC thesaurus added to additional patent databases on STN
NEWS 14 FEB 22 Updates in EPFULL; IPC 8 enhancements added
NEWS 15 FEB 27 New STN AnaVist pricing effective March 1, 2006
NEWS 16 FEB 28 MEDLINE/LMEDLINE reload improves functionality
NEWS 17 FEB 28 TOXCENTER reloaded with enhancements
NEWS 18 FEB 28 REGISTRY/ZREGISTRY enhanced with more experimental spectral
property data
NEWS 19 MAR 01 INSPEC reloaded and enhanced
NEWS 20 MAR 03 Updates in PATDPA; addition of IPC 8 data without attributes
NEWS 21 MAR 08 X.25 communication option no longer available after June 2006
NEWS 22 MAR 22 EMBASE is now updated on a daily basis

NEWS EXPRESS FEBRUARY 15 CURRENT VERSION FOR WINDOWS IS V8.01a,
CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
AND CURRENT DISCOVER FILE IS DATED 19 DECEMBER 2005.
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FILE 'HOME' ENTERED AT 10:40:31 ON 28 MAR 2006

=> file reg

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.21	0.21

FILE 'REGISTRY' ENTERED AT 10:40:42 ON 28 MAR 2006

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DICTIONARY FILE UPDATES: 27 MAR 2006 HIGHEST RN 878190-58-0

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* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*

Structure search iteration limits have been increased. See HELP SLIMITS for details.

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<http://www.cas.org/ONLINE/UG/regprops.html>

=> s TGAAATGCTCA/SQEN
2 TGAAATGCTCA/SQEN
87009 SQL=11
L1 2 TGAAATGCTCA/SQEN
(TGAAATGCTCA/SQEN AND SQL=11)

=> file caplus

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	7.93	8.14

FILE 'CAPLUS' ENTERED AT 10:41:37 ON 28 MAR 2006

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FILE COVERS 1907 - 28 Mar 2006 VOL 144 ISS 14
FILE LAST UPDATED: 27 Mar 2006 (20060327/ED)

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=> s l1

L2 1 L1

=> d ibib

L2 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2001:208447 CAPLUS

DOCUMENT NUMBER: 134:247984

TITLE: Polymorphisms in the human CYP3A4 and CYP3A7 genes and their use in diagnostic and therapeutic applications

INVENTOR(S): Wojnowski, Leszek; Eiselt, Regina

PATENT ASSIGNEE(S): Epidauros Biotechnologie A.-G., Germany

SOURCE: PCT Int. Appl., 106 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 3

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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WO 2001020025	A2	20010322	WO 2000-EP8570	20000901
WO 2001020025	A3	20011011		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
EP 1088900	A1	20010404	EP 1999-118120	19990910
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO			
CA 2379541	AA	20010322	CA 2000-2379541	20000901
EP 1210463	A2	20020605	EP 2000-964092	20000901
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL			
JP 2003509063	T2	20030311	JP 2001-523796	20000901

US 2002160479	A1	20021031	US 2001-7814	20011109
NO 2002001146	A	20020415	NO 2002-1146	20020307
PRIORITY APPLN. INFO.:			EP 1999-118120	A 19990910
			US 2000-583447	A3 20000530
			WO 2000-EP8570	W 20000901

=> file reg

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

FULL ESTIMATED COST

1.60

9.74

FILE 'REGISTRY' ENTERED AT 10:42:18 ON 28 MAR 2006

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DICTIONARY FILE UPDATES: 27 MAR 2006 HIGHEST RN 878190-58-0

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* the IDE default display format and the ED field has been added, *
* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*
*****

```

Structure search iteration limits have been increased. See HELP SLIMITS for details.

REGISTRY includes numerically searchable data for experimental and predicted properties as well as tags indicating availability of experimental property data in the original document. For information on property searching in REGISTRY, refer to:

<http://www.cas.org/ONLINE/UG/regprops.html>

=> s TGAAATGCTCA/SQSN

L3 26979 TGAAATGCTCA/SQSN

=> s l3 and SQL<=50

7659901 SQL<=50

L4 13 L3 AND SQL<=50

=> file caplus

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

FULL ESTIMATED COST

34.53

44.27

FILE 'CAPLUS' ENTERED AT 10:44:00 ON 28 MAR 2006

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FILE COVERS 1907 - 28 Mar 2006 VOL 144 ISS 14
FILE LAST UPDATED: 27 Mar 2006 (20060327/ED)

Effective October 17, 2005, revised CAS Information Use Policies apply. They are available for your review at:

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=> s l4
L5          10 L4

=> s l5 not py>1999
        6510150 PY>1999
L6          0 L5 NOT PY>1999

=> d l5 ibib 7-10
```

L5 ANSWER 7 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2004:633637 CAPLUS
DOCUMENT NUMBER: 141:152173
TITLE: Method and oligonucleotide probes for genotyping
polymorphisms in humans
INVENTOR(S): Matsuzaki, Hajime; Mei, Rui; Shen, Mei-Mei; Kennedy,
Giulia C.
PATENT ASSIGNEE(S): Affymetrix, Inc., USA
SOURCE: U.S. Pat. Appl. Publ., 13 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 26
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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US 2004146890	A1	20040729	US 2003-681773	20031007
US 2004146890	A1	20040729	US 2003-681773	20031007
PRIORITY APPLN. INFO.:			US 2002-417190P	P 20021008
			US 2003-470475P	P 20030514
			US 2003-681773	A 20031007

L5 ANSWER 8 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2004:120997 CAPLUS
DOCUMENT NUMBER: 140:158538
TITLE: Methods for detecting PrP gene polymorphisms
associated with scrapie in sheep using primer
extension
INVENTOR(S): Mckeown, Brian; Derbyshire, Roger; Rowan, Paul; Sung,

PATENT ASSIGNEE(S): Robert
 SOURCE: Orchid Biosciences, Inc., USA
 PCT Int. Appl., 121 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 2
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004013346	A2	20040212	WO 2003-US24198	20030801
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
US 2004121342	A1	20040624	US 2002-328150	20021220
CA 2497570	AA	20040212	CA 2003-2497570	20030801
EP 1576174	A2	20050921	EP 2003-767088	20030801
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK			
PRIORITY APPLN. INFO.:			US 2002-400533P	P 20020802
			US 2002-328150	A 20021220
			WO 2003-US24198	W 20030801

L5 ANSWER 9 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
 ACCESSION NUMBER: 2001:208447 CAPLUS
 DOCUMENT NUMBER: 134:247984
 TITLE: Polymorphisms in the human CYP3A4 and CYP3A7 genes and their use in diagnostic and therapeutic applications
 INVENTOR(S): Wojnowski, Leszek; Eiselt, Regina
 PATENT ASSIGNEE(S): Epidauros Biotechnologie A.-G., Germany
 SOURCE: PCT Int. Appl., 106 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 3
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001020025	A2	20010322	WO 2000-EP8570	20000901
WO 2001020025	A3	20011011		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
EP 1088900	A1	20010404	EP 1999-118120	19990910
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO			
CA 2379541	AA	20010322	CA 2000-2379541	20000901

EP 1210463 A2 20020605 EP 2000-964092 20000901
 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
 IE, SI, LT, LV, FI, RO, MK, CY, AL
 JP 2003509063 T2 20030311 JP 2001-523796 20000901
 US 2002160479 A1 20021031 US 2001-7814 20011109
 NO 2002001146 A 20020415 NO 2002-1146 20020307
 PRIORITY APPLN. INFO.: EP 1999-118120 A 19990910
 US 2000-583447 A3 20000530
 WO 2000-EP8570 W 20000901

L5 ANSWER 10 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2000:707338 CAPLUS

DOCUMENT NUMBER: 133:291967

TITLE: Single nucleotide polymorphisms in coding regions of
 human genes and primers/probes and methods for
 detection thereof

INVENTOR(S): Altshuler, David; Cargill, Michele; Daley, George Q.;
 Ireland, James S.; Lander, Eric S.; Lipshutz, Robert
 J.; Patil, Nila; Sklar, Pamela

PATENT ASSIGNEE(S): Whitehead Institute for Biomedical Research, USA;
 Affymetrix, Inc.

SOURCE: PCT Int. Appl., 216 pp.
 CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000058519	A2	20001005	WO 2000-US8440	20000330
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
PRIORITY APPLN. INFO.:			US 1999-127248P	P 19990331

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=> file re

'RE' IS AN AMBIGUOUS FILE OR CLUSTER NAME

REACTION - Reactions Cluster

RESEARCH - Research Cluster
REGISTRY - The CAS Registry File of substances
ENTER FILE OR CLUSTER NAME (IGNORE):end

=> file reg
COST IN U.S. DOLLARS SINCE FILE TOTAL
ENTRY SESSION
FULL ESTIMATED COST 0.21 0.21

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DICTIONARY FILE UPDATES: 27 MAR 2006 HIGHEST RN 878190-58-0

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on property searching in REGISTRY, refer to:

<http://www.cas.org/ONLINE/UG/regprops.html>

=> s TGAATGCTCA/SQSN
L1 26979 TGAATGCTCA/SQSN

=> s l1 and SQL,+50
0 SQL,+50
L2 0 L1 AND SQL,+50

=> s l1 and SQL<=50
7659901 SQL<=50
L3 13 L1 AND SQL<=50

=> file caplus
COST IN U.S. DOLLARS SINCE FILE TOTAL
ENTRY SESSION
FULL ESTIMATED COST 39.29 39.50

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FILE COVERS 1907 - 28 Mar 2006 VOL 144 ISS 14
 FILE LAST UPDATED: 27 Mar 2006 (20060327/ED)

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=> s l3
 L4 10 L3

=> d ibib 1-10

L4 ANSWER 1 OF 10 CAPLUS COPYRIGHT 2006 ACS ON STN
 ACCESSION NUMBER: 2005:1154714 CAPLUS
 DOCUMENT NUMBER: 143:438059
 TITLE: Genetic polymorphisms in 11 genes associated with an increased risk of osteoarthritis
 INVENTOR(S): Mah, Steven; Braun, Andreas; Kammerer, Stefan M.; Nelson, Matthew Roberts; Reneland, Rikard Henry; Langdown, Maria L.
 PATENT ASSIGNEE(S): Sequenom, Inc., USA
 SOURCE: PCT Int. Appl., 539 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2005100604	A2	20051027	WO 2005-US10912	20050331
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SM, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW			
RW:	BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
PRIORITY APPLN. INFO.:			US 2004-559011P	P 20040401
			US 2004-559040P	P 20040401
			US 2004-559042P	P 20040401

US 2004-559202P	P	20040401
US 2004-559203P	P	20040401
US 2004-559225P	P	20040401
US 2004-559275P	P	20040401

L4 ANSWER 2 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
 ACCESSION NUMBER: 2005:1004428 CAPLUS
 DOCUMENT NUMBER: 143:282819
 TITLE: Use of Solanum bulbocastanum genes RB, RGA1 RGA3 and RGA4 for conferring broad spectrum resistance to potato late blight in transgenic solanaceae
 INVENTOR(S): Helgeson, John Paul; Austin-Phillips, Sandra; Naess, Sara Kristine; Song, Junqi; Jiang, Jiming; Bradeen, James Mathew; Buell, C. Rubin
 PATENT ASSIGNEE(S): USA
 SOURCE: U.S. Pat. Appl. Publ., 121 pp.
 CODEN: USXXCO
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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US 2005204419	A1	20050915	US 2004-755966	20040112
PRIORITY APPLN. INFO.:			US 2003-439376P	P 20030110

L4 ANSWER 3 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
 ACCESSION NUMBER: 2005:172216 CAPLUS
 DOCUMENT NUMBER: 142:213372
 TITLE: Oligonucleotide probes for analysis of gene expression in mouse
 INVENTOR(S): Zhou, Xue Mei
 PATENT ASSIGNEE(S): Affymetrix, Inc., USA
 SOURCE: U.S. Pat. Appl. Publ., 13 pp.
 CODEN: USXXCO
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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US 2005026164 A1		20050203	US 2003-XC719900	20031120
PRIORITY APPLN. INFO.:			US 2002-2002/PV42780U	20021120
			US 2003-2003/719900	20031120

L4 ANSWER 4 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
 ACCESSION NUMBER: 2005:110603 CAPLUS
 DOCUMENT NUMBER: 142:171061
 TITLE: Oligonucleotide probes for analysis of gene expression in mouse
 INVENTOR(S): Zhou, Xue Mei
 PATENT ASSIGNEE(S): Affymetrix, Inc., USA
 SOURCE: U.S. Pat. Appl. Publ., 13 pp.
 CODEN: USXXCO
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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US 2005026164 A1		20050203	US 2003-XS719900	20031120

PRIORITY APPLN. INFO.: US 2002-2002/PV42780U 20021120
US 2003-2003/719900 20031120

L4 ANSWER 5 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2004:701704 CAPLUS
DOCUMENT NUMBER: 141:219946
TITLE: Methods for genotyping scrapie-resistant sheep
populations
INVENTOR(S): McKeown, Brian; Derbyshire, Roger; Rowan, Paul; Sung,
Robert
PATENT ASSIGNEE(S): Orchid Biosciences, Inc., USA
SOURCE: U.S. Pat. Appl. Publ., 64 pp., Cont.-in-part of U.S.
Ser. No. 328,150.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2004166506	A1	20040826	US 2003-632393	20030801
US 2004121342	A1	20040624	US 2002-328150	20021220
PRIORITY APPLN. INFO.:			US 2002-400533P	P 20020802
			US 2002-328150	A2 20021220

L4 ANSWER 6 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2004:633648 CAPLUS
DOCUMENT NUMBER: 141:135193
TITLE: Method and oligonucleotide probes for genotyping
polymorphisms in humans
INVENTOR(S): Matsuzaki, Hajime; Mei, Rui; Shen, Mei-Mei; Kennedy,
Giulia C.
PATENT ASSIGNEE(S): Affymetrix, Inc., USA
SOURCE: U.S. Pat. Appl. Publ., 13 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 26
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2004146890	A1	20040729	US 2003-681773	20031007
US 2004146890	A1	20040729	US 2003-681773	20031007
PRIORITY APPLN. INFO.:			US 2002-417190P	P 20021008
			US 2003-470475P	P 20030514
			US 2003-681773	A 20031007

L4 ANSWER 7 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2004:633637 CAPLUS
DOCUMENT NUMBER: 141:152173
TITLE: Method and oligonucleotide probes for genotyping
polymorphisms in humans
INVENTOR(S): Matsuzaki, Hajime; Mei, Rui; Shen, Mei-Mei; Kennedy,
Giulia C.
PATENT ASSIGNEE(S): Affymetrix, Inc., USA
SOURCE: U.S. Pat. Appl. Publ., 13 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 26

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2004146890	A1	20040729	US 2003-681773	20031007
US 2004146890	A1	20040729	US 2003-681773	20031007
PRIORITY APPLN. INFO.:			US 2002-417190P	P 20021008
			US 2003-470475P	P 20030514
			US 2003-681773	A 20031007

L4 ANSWER 8 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
 ACCESSION NUMBER: 2004:120997 CAPLUS
 DOCUMENT NUMBER: 140:158538
 TITLE: Methods for detecting PrP gene polymorphisms associated with scrapie in sheep using primer extension
 INVENTOR(S): Mckeown, Brian; Derbyshire, Roger; Rowan, Paul; Sung, Robert
 PATENT ASSIGNEE(S): Orchid Biosciences, Inc., USA
 SOURCE: PCT Int. Appl., 121 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 2
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004013346	A2	20040212	WO 2003-US24198	20030801
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 2004121342	A1	20040624	US 2002-328150	20021220
CA 2497570	AA	20040212	CA 2003-2497570	20030801
EP 1576174	A2	20050921	EP 2003-767088	20030801
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK				
PRIORITY APPLN. INFO.:			US 2002-400533P	P 20020802
			US 2002-328150	A 20021220
			WO 2003-US24198	W 20030801

L4 ANSWER 9 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
 ACCESSION NUMBER: 2001:208447 CAPLUS
 DOCUMENT NUMBER: 134:247984
 TITLE: Polymorphisms in the human CYP3A4 and CYP3A7 genes and their use in diagnostic and therapeutic applications
 INVENTOR(S): Wojnowski, Leszek; Eiselt, Regina
 PATENT ASSIGNEE(S): Epidauros Biotechnologie A.-G., Germany
 SOURCE: PCT Int. Appl., 106 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 3
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001020025	A2	20010322	WO 2000-EP8570	20000901
WO 2001020025	A3	20011011		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
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EP 1088900	A1	20010404	EP 1999-118120	19990910
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CA 2379541	AA	20010322	CA 2000-2379541	20000901
EP 1210463	A2	20020605	EP 2000-964092	20000901
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JP 2003509063	T2	20030311	JP 2001-523796	20000901
US 2002160479	A1	20021031	US 2001-7814	20011109
NO 2002001146	A	20020415	NO 2002-1146	20020307
PRIORITY APPLN. INFO.:			EP 1999-118120	A 19990910
			US 2000-583447	A3 20000530
			WO 2000-EP8570	W 20000901

L4 ANSWER 10 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2000:707338 CAPLUS

DOCUMENT NUMBER: 133:291967

TITLE: Single nucleotide polymorphisms in coding regions of human genes and primers/probes and methods for detection thereof

INVENTOR(S): Altshuler, David; Cargill, Michele; Daley, George Q.; Ireland, James S.; Lander, Eric S.; Lipshutz, Robert J.; Patil, Nila; Sklar, Pamela

PATENT ASSIGNEE(S): Whitehead Institute for Biomedical Research, USA; Affymetrix, Inc.

SOURCE: PCT Int. Appl., 216 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000058519	A2	20001005	WO 2000-US8440	20000330
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
PRIORITY APPLN. INFO.:			US 1999-127248P	P 19990331

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L5 26 US 6821724/PN

(US6821724/PN)

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PASSWORD:

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NEWS	3	JAN 16	CAS patent coverage enhanced to include exemplified prophetic substances
NEWS	4	JAN 28	USPATFULL, USPAT2, and USPATOLD enhanced with new custom IPC display formats
NEWS	5	JAN 28	MARPAT searching enhanced
NEWS	6	JAN 28	USGENE now provides USPTO sequence data within 3 days of publication
NEWS	7	JAN 28	TOXCENTER enhanced with reloaded MEDLINE segment
NEWS	8	JAN 28	MEDLINE and LMEDLINE reloaded with enhancements
NEWS	9	FEB 08	STN Express, Version 8.3, now available
NEWS	10	FEB 20	PCI now available as a replacement to DPCI
NEWS	11	FEB 25	IFIREF reloaded with enhancements
NEWS	12	FEB 25	IMSPRODUCT reloaded with enhancements
NEWS	13	FEB 29	WPINDEX/WPIDS/WPIX enhanced with ECLA and current U.S. National Patent Classification

NEWS 14 MAR 31 IFICDB, IFIPAT, and IFIUDB enhanced with new custom
IPC display formats

NEWS 15 MAR 31 CAS REGISTRY enhanced with additional experimental
spectra

NEWS 16 MAR 31 CA/Caplus and CASREACT patent number format for U.S.
applications updated

NEWS 17 MAR 31 LPCI now available as a replacement to LDPCI

NEWS 18 MAR 31 EMBASE, EMBAL, and LEMBASE reloaded with enhancements

NEWS 19 APR 04 STN AnaVist, Version 1, to be discontinued

NEWS 20 APR 15 WPIDS, WPINDEX, and WPIX enhanced with new
predefined hit display formats

NEWS 21 APR 28 EMBASE Controlled Term thesaurus enhanced

NEWS 22 APR 28 IMSRESEARCH reloaded with enhancements

NEWS 23 MAY 30 INPAFAMDB now available on STN for patent family
searching

NEWS 24 MAY 30 DGENE, PCTGEN, and USGENE enhanced with new homology
sequence search option

NEWS 25 JUN 06 EPFULL enhanced with 260,000 English abstracts

NEWS 26 JUN 06 KOREAPAT updated with 41,000 documents

NEWS 27 JUN 13 USPATFULL and USPAT2 updated with 11-character
patent numbers for U.S. applications

NEWS 28 JUN 19 CAS REGISTRY includes selected substances from
web-based collections

NEWS 29 JUN 25 CA/Caplus and USPAT databases updated with IPC
reclassification data

NEWS 30 JUN 30 AEROSPACE enhanced with more than 1 million U.S.
patent records

NEWS 31 JUN 30 EMBASE, EMBAL, and LEMBASE updated with additional
options to display authors and affiliated
organizations

NEWS 32 JUN 30 STN on the Web enhanced with new STN AnaVist
Assistant and BLAST plug-in

NEWS 33 JUN 30 STN AnaVist enhanced with database content from EPFULL

NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,
AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.

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COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	0.21	0.21

FILE 'REGISTRY' ENTERED AT 14:08:05 ON 21 JUL 2008
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DICTIONARY FILE UPDATES: 20 JUL 2008 HIGHEST RN 1035004-20-6

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=> s ATGAAATGCTCAGAT/sqsn
L2 141 ATGAAATGCTCAGAT/SQSN

=> s AATGAAATGCTCAGA/sqsn
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L5 144 TGAATGAAATGCTCA/SQSN

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L6 493 L1 OR L2 OR L3 OR L4 OR L5

=> s l6 and SQL<=50
8681680 SQL<=50
L7 1 L6 AND SQL<=50

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SINCE FILE	TOTAL
ENTRY	SESSION
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FULL ESTIMATED COST

FILE 'CAPLUS' ENTERED AT 14:14:59 ON 21 JUL 2008
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FILE LAST UPDATED: 20 Jul 2008 (20080720/ED)

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=> s l7

L8 1 L7

=> d ibib abs

L8 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2008 ACS on SIN

ACCESSION NUMBER: 2007:1280786 CAPLUS

DOCUMENT NUMBER: 148:25140

TITLE: Detecting cytochrome 3A gene by nucleic acid hybridization using biochip

INVENTOR(S): Sheng, Haihui; Xiao, Huasheng

PATENT ASSIGNEE(S): Shanghai Biochip Co., Ltd., Peop. Rep. China

SOURCE: Faming Zhuanli Shenqing Gongkai Shuomingshu, 39pp.

CODEN: CNXXEV

DOCUMENT TYPE: Patent

LANGUAGE: Chinese

FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
CN 101067149	A	20071107	CN 2006-10119553	20061213
WO 2008011787	A1	20080131	WO 2007-CN1853	20070612
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BH, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, SV, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW			
RW:	AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, LV, MC, MT, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG, BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			

PRIORITY APPLN. INFO.: CN 2006-10029005 A 20060717
CN 2006-10119553 A 20061213

AB This invention relates to a method for detecting the cytochrome 3A gene in species, including human, by nucleic acid hybridization using CYT3A gene-specific biochips. The probes can hybridize with nucleotide sequence and/or complementary sequence of cytochrome 3A (CYP3A) gene. The invention provides the sequences of the DNA probes affixed on the chips. The CYP3A chip can be used for detecting CYP3A gene mutation in clinic, typing CYP3A4, CYP3A5 and CYP3A7 genes, evaluating effects of drugs.

=> d his

(FILE 'HOME' ENTERED AT 14:07:44 ON 21 JUL 2008)

FILE 'REGISTRY' ENTERED AT 14:08:05 ON 21 JUL 2008

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L3 129 S AATGAAATGCTCAGA/SQSN
L4 88 S GAATGAAATGCTCAG/SQSN
L5 144 S TGAATGAAATGCTCA/SQSN
L6 493 S L1 OR L2 OR L3 OR L4 OR L5
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L9 146 L6

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L10 7 L9 NOT PY>2000

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L10 ANSWER 1 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2000:767749 CAPLUS

DOCUMENT NUMBER: 133:318131

TITLE: Characterization and repeat analysis of the compact genome of the freshwater pufferfish *Tetraodon nigroviridis*

AUTHOR(S): Crolius, H. Roest; Jaillon, O.; Dasilva, C.; Ozouf-Costaz, C.; Fizames, C.; Fischer, C.; Bouneau, L.; Billault, A.; Quetier, F.; Saurin, W.; Bernot, A.; Weissenbach, J.

CORPORATE SOURCE: Genoscope, Evry, 91057, Fr.
SOURCE: Genome Research (2000), 10(7), 939-949

CODEN: GEREFS; ISSN: 1088-9051

PUBLISHER: Cold Spring Harbor Laboratory Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB *Tetraodon nigroviridis* is a freshwater pufferfish 20-30 million years distant from *Fugu rubripes*. The genome of both tetraodontiforms is compact, mostly because intergenic and intronic sequences are reduced in size compared to other vertebrate genomes. The previously uncharacterized *Tetraodon* genome is described here together with a detailed anal. of its repeat content and organization. The sequencing of 46 megabases of bacterial artificial chromosome (BAC) end sequences is reported, which represents a random DNA sample equivalent to 13% of the genome. The sequence and location of rRNA gene clusters, centromeric and subtelocentric satellite sequences were determined. Minisatellites and microsatellites were cataloged and notable differences were observed in comparison with microsatellites from *Fugu*. The genome contains homologies to all known families of transposable elements, including Ty3-gypsy, Ty1-copia, Line retrotransposons, DNA transposons, and retroviruses, although their overall abundance is <1%. This structural anal. is an important prerequisite to sequencing the *Tetraodon* genome. [This abstract record is one of 10 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

L10 ANSWER 2 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2000:767717 CAPLUS

DOCUMENT NUMBER: 133:318128

TITLE: Characterization and repeat analysis of the compact genome of the freshwater pufferfish *Tetraodon nigroviridis*

AUTHOR(S): Crollius, H. Roest; Jaillon, O.; Dasilva, C.; Ozouf-Costaz, C.; Fizames, C.; Fischer, C.; Bouneau, L.; Billault, A.; Quetier, F.; Saurin, W.; Bernot, A.; Weissenbach, J.

CORPORATE SOURCE: Genoscope, Evry, 91057, Fr.

SOURCE: Genome Research (2000), 10(7), 939-949
CODEN: GEREFS; ISSN: 1088-9051

PUBLISHER: Cold Spring Harbor Laboratory Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB *Tetraodon nigroviridis* is a freshwater pufferfish 20-30 million years distant from *Fugu rubripes*. The genome of both tetraodontiforms is compact, mostly because intergenic and intronic sequences are reduced in size compared to other vertebrate genomes. The previously uncharacterized *Tetraodon* genome is described here together with a detailed anal. of its repeat content and organization. The sequencing of 46 megabases of bacterial artificial chromosome (BAC) end sequences is reported, which represents a random DNA sample equivalent to 13% of the genome. The sequence and location of rRNA gene clusters, centromeric and subtelocentric satellite sequences were determined. Minisatellites and microsatellites were cataloged and notable differences were observed in comparison with microsatellites from *Fugu*. The genome contains homologies to all known families of transposable elements, including Ty3-gypsy, Ty1-copia, Line retrotransposons, DNA transposons, and retroviruses, although their overall abundance is <1%. This structural anal. is an important prerequisite to sequencing the *Tetraodon* genome. [This abstract record is one of 10 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

L10 ANSWER 3 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2000:611831 CAPLUS

DOCUMENT NUMBER: 133:233401

TITLE: A sea urchin genome project: sequence scan, virtual map, and additional resources

AUTHOR(S): Cameron, R. Andrew; Mahairas, Gregory; Rast, Jonathan P.; Martinez, Pedro; Biondi, Ted R.; Swartzell, Steven; Wallace, James C.; Poustka, Albert J.; Livingston, Brian T.; Wray, Gregory A.; Etensohn, Charles A.; Lehrach, Hans; Britten, Roy J.; Davidson, Eric H.; Hood, Leroy

CORPORATE SOURCE: Stowers Inst. Med. Res., Kansas City, MO, 64110, USA

SOURCE: Proceedings of the National Academy of Sciences of the United States of America (2000), 97(17), 9514-9518
CODEN: PNASA6; ISSN: 0027-8424

PUBLISHER: National Academy of Sciences

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Results of a first-stage Sea Urchin Genome Project are summarized. The species chosen was *Strongylocentrotus purpuratus*, a research model of major importance in developmental and mol. biol. A virtual map of the genome was constructed by sequencing the ends of 76,020 bacterial artificial chromosome (BAC) recombinants (average length, 125 kb). The BAC-end sequence tag connectors (STCs) occur an average of 10 kb apart, and, together with restriction digest patterns recorded for the same BAC clones, they provide immediate access to contigs of several hundred kilobases surrounding any gene of interest. The STCs survey >5% of the genome and provide the estimate that this genome contains ~27,350 protein-coding genes. The frequency distribution and canonical sequences

of all middle and highly repetitive sequence families in the genome were obtained from the STCs as well. The 500-kb Hox gene complex of this species is being sequenced in its entirety. In addition, arrayed cDNA libraries of >105 clones each were constructed from every major stage of embryogenesis, several individual cell types, and adult tissues and are available to the community. The accumulated STC data (AZ135866-AZ211804) and an expanding expressed sequence tag database (at present including >12,000 sequences) have been reported to GenBank and are accessible on public web sites. [This abstract record is one of 19 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints].

L10 ANSWER 4 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2000:366621 CAPLUS
DOCUMENT NUMBER: 132:344010
TITLE: The DNA sequence of human chromosome 21
AUTHOR(S): Hattori, M.; Fujiyama, A.; Taylor, T. D.; Watanabe, H.; Yada, T.; Park, H.-S.; Toyoda, A.; Ishii, K.; Totoki, Y.; Choi, D.-K.; Soeda, E.; Ohki, M.; Takagi, T.; Sakaki, Y.; Taudien, S.; Blechschmidt, K.; Polley, A.; Menzel, U.; Delabar, J.; Kumpf, K.; Lehmann, R.; Patterson, D.; Reichwald, K.; Rump, A.; Schillhabel, M.; Schudy, A.; Zimmermann, W.; Rosenthal, A.; Kudoh, J.; Shibuya, K.; Kawasaki, K.; Asakawa, S.; Shintani, A.; Sasaki, T.; Nagamine, K.; Mitsuyama, S.; Antonarakis, S. E.; Minoshima, S.; Shimizu, N.; Nordsiek, G.; Hornischer, K.; Brandt, P.; Scharfe, M.; Schon, O.; Desario, A.; Reichelt, J.; Kauer, G.; Blocker, H.; Ramser, J.; Beck, A.; Klages, S.; Hennig, S.; Riesselmann, L.; Dagand, E.; Haaf, T.; Wehrmeyer, S.; Borzym, K.; Gardiner, K.; Nizetic, D.; Francis, F.; Lehrach, H.; Reinhardt, R.; Yaspo, M.-L.
CORPORATE SOURCE: Genomic Sciences Center, RIKEN, Sagamihara, 228-8555, Japan
SOURCE: Nature (London) (2000), 405(6784), 311-319
CODEN: NATUAS; ISSN: 0028-0836
PUBLISHER: Nature Publishing Group
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Chromosome 21 is the smallest human autosome. An extra copy of chromosome 21 causes Down syndrome, the most frequent genetic cause of significant mental retardation, which affects up to 1 in 700 live births. Several anonymous loci for monogenic disorders and predispositions for common complex disorders have also been mapped to this chromosome, and loss of heterozygosity has been observed in regions associated with solid tumors. This report provides the sequence and gene catalog of the long arm of chromosome 21. At least 33,546,361 base pairs (bp) of DNA have been sequenced with very high accuracy, the largest contig being 25,491,867 bp. Only 3 small clone gaps and 7 sequencing gaps remain, comprising .apprx.100 kilobases. Thus, 99.7% coverage of 21q was achieved. About 281,116 bp were also sequenced from the short arm. The structural features identified include duplications that are probably involved in chromosomal abnormalities and repeat structures in the telomeric and pericentromeric regions. Anal. of the chromosome revealed 127 known genes, 98 predicted genes and 59 pseudogenes. The sequences are deposited in the GenBank database, and addnl. information can be found from the home pages of the participating centers of the chromosome 21 sequencing consortium.

REFERENCE COUNT: 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 5 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER:
DOCUMENT NUMBER:
TITLE:
AUTHOR(S):

2000:246921 CAPLUS
132:275067

The genome sequence of *Drosophila melanogaster*
Adams, Mark D.; Celniker, Susan E.; Holt, Robert A.;
Evans, Cheryl A.; Gocayne, Jeannine D.; Amanatides,
Peter G.; Scherer, Steven E.; Li, Peter W.; Hoskins,
Roger A.; Galle, Richard F.; George, Reed A.; Lewis,
Suzanna E.; Richards, Stephen; Ashburner, Michael;
Henderson, Scott N.; Sutton, Granger G.; Wortman,
Jennifer R.; Yandell, Mark D.; Zhang, Qing; Chen, Lin
X.; Brandon, Rhonda C.; Rogers, Yu-Hui C.; Blazej,
Robert G.; Champe, Mark; Pfeiffer, Barret D.; Wan,
Kenneth H.; Doyle, Clare; Baxter, Evan G.; Helt,
Gregg; Nelson, Catherine R.; Miklos, George L. Gabor;
Abril, Josep F.; Agbayani, Anna; An, Hui-Jin;
Andrews-Pfannkoch, Cynthia; Baldwin, Danita; Ballew,
Richard M.; Basu, Anand; Baxendale, James;
Bayraktaroglu, Leyla; Beasley, Ellen M.; Beeson, Karen
Y.; Benos, P. V.; Berman, Benjamin P.; Bhandari,
Deepali; Bolshakov, Slava; Borkova, Dana; Botchan,
Michael R.; Bouck, John; Brokstein, Peter; Brottier,
Phillipe; Burtis, Kenneth C.; Busam, Dana A.; Butler,
Heather; Cadieu, Edouard; Center, Angela; Chandra,
Ishwar; Cherry, J. Michael; Cawley, Simon; Dahlke,
Carl; Davenport, Lionel B.; Davies, Peter; De Pablos,
Beatriz; Delcher, Arthur; Deng, Zuoming; Mays, Anne
Deslattes; Dew, Ian; Dietz, Suzanne M.; Dodson,
Kristina; Doup, Lisa E.; Downes, Michael; Dugan-Rocha,
Shannon; Dunkov, Boris C.; Dunn, Patrick; Durbin,
Kenneth J.; Evangelista, Carlos C.; Ferraz,
Concepcion; Ferriera, Steven; Fleischmann, Wolfgang;
Foster, Carl; Gabrielian, Andrei E.; Garg, Neha S.;
Gelbart, William M.; Glasser, Ken; Glodek, Anna; Gong,
Fangcheng; Gorrell, J. Harley; Gu, Zhiping; Guan,
Ping; Harris, Michael; Harris, Nomi L.; Harvey, Damon;
Heiman, Thomas J.; Hernandez, Judith R.; Houck,
Jarrett; Hostin, Damon; Houston, Kathryn A.; Howland,
Timothy J.; Wei, Ming-Hui; Ibegwam, Chinyere; Jalali,
Mena; Kalush, Francis; Karpen, Gary H.; Ke, Zhaoxi;
Kennison, James A.; Ketchum, Karen A.; Kimmel, Bruce
E.; Kodira, Chinnappa D.; Kraft, Cheryl; Kravitz,
Saul; Kulp, David; Lai, Zhongwu; Lasko, Paul; Lei,
Yiding; Levitsky, Alexander A.; Li, Jiayin; Li,
Zhenya; Liang, Yong; Lin, Xiaoying; Liu, Xiangjun;
Mattel, Bettina; McIntosh, Tina C.; McLeod, Michael
P.; McPherson, Duncan; Merkulov, Gennady; Milshina,
Natalia V.; Mobarrey, Clark; Morris, Joe; Moshrefi,
Ali; Mount, Stephen M.; Moy, Mee; Murphy, Brian;
Murphy, Lee; Muzny, Donna M.; Nelson, David L.;
Nelson, David R.; Nelson, Keith A.; Nixon, Katherine;
Nusskern, Deborah R.; Pacleb, Joanne M.; Palazzolo,
Michael; Pittman, Gjange S.; Pan, Sue; Pollard, John;
Puri, Vinita; Reese, Martin G.; Reinert, Knut;
Remington, Karin; Saunders, Robert D. C.; Scheeler,
Frederick; Shen, Hua; Shue, Bixiang Christopher;
Siden-Kiamos, Inga; Simpson, Michael; Skupski, Marian
P.; Smith, Tom; Spier, Eugene; Spradling, Allan C.;
Stapleton, Mark; Strong, Renee; Sun, Eric; Svirskas,
Robert; Tector, Cyndee; Turner, Russell; Venter, Eli;
Wang, Aihui H.; Wang, Xin; Wang, Zhen-Yuan; Wassarman,
David A.; Weinstock, George M.; Weissbach, Jean;
Williams, Sherita M.; Woodage, Trevor; Worley, Kim C.;

Wu, David; Yang, Song; Yao, Q. Alison; Ye, Jane; Yeh, Ru-Fang; Zaveri, Jayshree S.; Zhan, Ming; Zhang, Guangren; Zhao, Qi; Zheng, Liansheng; Zheng, Xiangqun H.; Zhong, Fei N.; Zhong, Wenyan; Zhou, Xiaojun; Zhu, Shiaoping; Zhu, Xiaohong; Smith, Hamilton O.; Gibbs, Richard A.; Myers, Eugene W.; Rubin, Gerald M.; Venter, J. Craig

CORPORATE SOURCE: Celera Genomics, Rockville, MD, 20850, USA
SOURCE: Science (Washington, D. C.) (2000), 287(5461), 2185-2195

CODEN: SCIEAS; ISSN: 0036-8075

PUBLISHER: American Association for the Advancement of Science

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The fly *Drosophila melanogaster* is one of the most intensively studied organisms in biol. and serves as a model system for the investigation of many developmental and cellular processes common to higher eukaryotes, including humans. The nucleotide sequence was determined of nearly all of the .apprx.120-megabase euchromatic portion of the *Drosophila* genome using a whole-genome shotgun sequencing strategy supported by extensive clone-based sequence and a high-quality bacterial artificial chromosome phys. map. Efforts are under way to close the remaining gaps; however, the sequence is of sufficient accuracy and contiguity to be declared substantially complete and to support an initial anal. of genome structure and preliminary gene annotation and interpretation. The genome encodes .apprx.13,600 genes, somewhat fewer than the smaller *Caenorhabditis elegans* genome, but with comparable functional diversity. Access to supporting information on each gene is available through FlyBase at <http://flybase.bio.indiana.edu> and through Celera at www.celera.com; the sequences are deposited in GenBank with Accession Nos. AE002566-AE003403. [This abstract record is one of 4 records for this document necessitated by the large number of index entries required to fully index the document and publication system restraints.].

L10 ANSWER 6 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2000:246831 CAPLUS

DOCUMENT NUMBER: 132:275066

TITLE: The genome sequence of *Drosophila melanogaster*

AUTHOR(S): Adams, Mark D.; Celniker, Susan E.; Holt, Robert A.; Evans, Cheryl A.; Gocayne, Jeannine D.; Amanatides, Peter G.; Scherer, Steven E.; Li, Peter W.; Hoskins, Roger A.; Galle, Richard F.; George, Reed A.; Lewis, Suzanna E.; Richards, Stephen; Ashburner, Michael; Henderson, Scott N.; Sutton, Granger G.; Wortman, Jennifer R.; Yandell, Mark D.; Zhang, Qing; Chen, Lin X.; Brandon, Rhonda C.; Rogers, Yu-Hui C.; Blazej, Robert G.; Champe, Mark; Pfeiffer, Barret D.; Wan, Kenneth H.; Doyle, Clare; Baxter, Evan G.; Helt, Gregg; Nelson, Catherine R.; Miklos, George L. Gabor; Abril, Josep F.; Agbayani, Anna; An, Hui-Jin; Andrews-Pfannkoch, Cynthia; Baldwin, Danita; Ballew, Richard M.; Basu, Anand; Baxendale, James; Bayraktaroglu, Leyla; Beasley, Ellen M.; Beeson, Karen Y.; Benos, P. V.; Berman, Benjamin P.; Bhandari, Deepali; Bolshakov, Slava; Borkova, Dana; Botchan, Michael R.; Bouck, John; Brokstein, Peter; Brottier, Philippe; Burtis, Kenneth C.; Busam, Dana A.; Butler, Heather; Cadieu, Edouard; Center, Angela; Chandra, Ishwar; Cherry, J. Michael; Cawley, Simon; Dahlke, Carl; Davenport, Lionel B.; Davies, Peter; De Pablos, Beatriz De; Delcher, Arthur; Deng, Zuoming; Mays, Anne Deslattes; Dew, Ian; Dietz, Suzanne M.; Dodson,

Kristina; Doup, Lisa E.; Downes, Michael; Dugan-Rocha, Shannon; Dunkov, Boris C.; Dunn, Patrick; Durbin, Kenneth J.; Evangelista, Carlos C.; Ferraz, Concepcion; Ferriera, Steven; Fleischmann, Wolfgang; Foster, Carl; Gabrielian, Andrei E.; Garg, Neha S.; Gelbart, William M.; Glasser, Ken; Glodek, Anna; Gong, Fangcheng; Gorrell, J. Harley; Gu, Zhiping; Guan, Ping; Harris, Michael; Harris, Nomi L.; Harvey, Damon; Heiman, Thomas J.; Hernandez, Judith R.; Houck, Jarrett; Hostin, Damon; Houston, Kathryn A.; Howland, Timothy J.; Wei, Ming-Hui; Ibegwam, Chinyere; Jalali, Mena; Kalush, Francis; Karpen, Gary H.; Ke, Zhaoxi; Kennison, James A.; Ketchum, Karen A.; Kimmel, Bruce E.; Kodira, Chinnappa D.; Kraft, Cheryl; Kravitz, Saul; Kulp, David; Lai, Zhongwu; Lasko, Paul; Lei, Yiding; Levitsky, Alexander A.; Li, Jiayin; Li, Zhenya; Liang, Yong; Lin, Xiaoying; Liu, Xiangjun; Mattel, Bettina; McIntosh, Tina C.; McLeod, Michael P.; McPherson, Duncan; Merkulov, Gennady; Milshina, Natalia V.; Mobarri, Clark; Morris, Joe; Moshrefi, Ali; Mount, Stephen M.; Moy, Mee; Murphy, Brian; Murphy, Lee; Muzny, Donna M.; Nelson, David L.; Nelson, David R.; Nelson, Keith A.; Nixon, Katherine; Nusskern, Deborah R.; Pacleb, Joanne M.; Palazzolo, Michael; Pittman, Gjange S.; Pan, Sue; Pollard, John; Puri, Vinita; Reese, Martin G.; Reinert, Knut; Remington, Karin; Saunders, Robert D. C.; Scheeler, Frederick; Shen, Hua; Shue, Bixiang Christopher; Siden-Kiamos, Inga; Simpson, Michael; Skupski, Marian P.; Smith, Tom; Spier, Eugene; Spradling, Allan C.; Stapleton, Mark; Strong, Renee; Sun, Eric; Svirskas, Robert; Tector, Cyndee; Turner, Russell; Venter, Eli; Wang, Aihui H.; Wang, Xin; Wang, Zhen-Yuan; Wassarman, David A.; Weinstock, George M.; Weissbach, Jean; Williams, Sherita M.; Woodage, Trevor; Worley, Kim C.; Wu, David; Yang, Song; Yao, Q. Alison; Ye, Jane; Yeh, Ru-Fang; Zaveri, Jayshree S.; Zhan, Ming; Zhang, Guangren; Zhao, Qi; Zheng, Liansheng; Zheng, Xiangqun H.; Zhong, Fei N.; Zhong, Wenyan; Zhou, Xiaojun; Zhu, Shiaoqing; Zhu, Xiaohong; Smith, Hamilton O.; Gibbs, Richard A.; Myers, Eugene W.; Rubin, Gerald M.; Venter, J. Craig

CORPORATE SOURCE: Celera Genomics, Rockville, MD, 20850, USA

SOURCE: Science (Washington, D. C.) (2000), 287(5461), 2185-2195

CODEN: SCIEAS; ISSN: 0036-8075

PUBLISHER: American Association for the Advancement of Science

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The fly *Drosophila melanogaster* is one of the most intensively studied organisms in biol. and serves as a model system for the investigation of many developmental and cellular processes common to higher eukaryotes, including humans. The nucleotide sequence was determined of nearly all of the .apprx.120-megabase euchromatic portion of the *Drosophila* genome using a whole-genome shotgun sequencing strategy supported by extensive clone-based sequence and a high-quality bacterial artificial chromosome phys. map. Efforts are under way to close the remaining gaps; however, the sequence is of sufficient accuracy and contiguity to be declared substantially complete and to support an initial anal. of genome structure and preliminary gene annotation and interpretation. The genome encodes .apprx.13,600 genes, somewhat fewer than the smaller *Caenorhabditis elegans* genome, but with comparable functional diversity. Access to

supporting information on each gene is available through FlyBase at <http://flybase.bio.indiana.edu> and through Celera at www.celera.com; the sequences are deposited in GenBank with Accession Nos. AE002566-AE003403. [This abstract record is one of 4 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

L10 ANSWER 7 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2000:47778 CAPLUS

DOCUMENT NUMBER: 132:118215

TITLE: Generation and analysis of 25 Mb of genomic DNA from

AUTHOR(S): the pufferfish *Fugu rubripes* by sequence scanning
Elgar, Greg; Clark, Melody S.; Meek, Stephen; Smith, Sarah; Warner, Sarah; Edwards, Yvonne J. K.; Bouchireb, Nassima; Cottage, Amanda; Yeo, Giles S. H.; Umrana, Yagnesh; Williams, Gary; Brenner, Sydney

CORPORATE SOURCE: UK Human Genome Mapping Project (HGMP) Resource

SOURCE: Centre, Hinxton, Cambridge, CB10 1SB, UK

Genome Research (1999), 9(10), 960-971

CODEN: GEREFS; ISSN: 1088-9051

PUBLISHER: Cold Spring Harbor Laboratory Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Over 50,000 shotgun clones were generated and analyzed from 1059 *Fugu* cosmid clones. All sequences have been minimally edited and searched against protein and DNA databases. These data are all displayed on a searchable, publicly available web site at <http://fugu.hgmp.mrc.ac.uk/>. With an average of 50 reads per cosmid, this is virtually nonredundant sequence skimming, covering 30%-50% of each clone. This essentially random data set covers nearly 25 Mb (>6%) of the *Fugu* genome and forms the basis of a series of whole genome analyses which address questions regarding gene d. and distribution in the *Fugu* genome and the similarity between *Fugu* and mammalian genes. The *Fugu* genome, with 8-fold less DNA but a similar gene repertoire, is ideally suited to this type of study because most cosmids contain more than one identifiable gene. General features of the genome are also discussed. Some estimation was made of the syntenic relationship between mammals and *Fugu* and the efficacy of ORF prediction from short, unedited *Fugu* genomic sequences studied. Comparative DNA sequence analyses are an essential tool in the functional interpretation of complex vertebrate genomes. This project highlights the utility of using the *Fugu* genome in this kind of study. [This abstract record is the third of 10 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

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DALL ----- ALL, delimited (end of each field identified)

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FBIB ----- AN, BIB, plus Patent FAM

IND ----- Indexing data
 IPC ----- International Patent Classifications
 MAX ----- ALL, plus Patent FAM, RE
 PATS ----- PI, SO
 SAM ----- CC, SX, TI, ST, IT
 SCAN ----- CC, SX, TI, ST, IT (random display, no answer numbers;
 SCAN must be entered on the same line as the DISPLAY,
 e.g., D SCAN or DISPLAY SCAN)
 STD ----- BIB, CLASS

 IABS ----- ABS, indented with text labels
 IALL ----- ALL, indented with text labels
 IBIB ----- BIB, indented with text labels
 IMAX ----- MAX, indented with text labels
 ISTD ----- STD, indented with text labels

 OBIB ----- AN, plus Bibliographic Data (original)
 OIBIB ----- OBIB, indented with text labels

 SBIB ----- BIB, no citations
 SIBIB ----- IBIB, no citations

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 HITIND ----- IC, ICA, ICI, NCL, CC and index field (ST and IT)
 containing hit terms
 HITRN ----- HIT RN and its text modification
 HITSTR ----- HIT RN, its text modification, its CA index name, and
 its structure diagram
 HITSEQ ----- HIT RN, its text modification, its CA index name, its
 structure diagram, plus NTE and SEQ fields
 FHITSTR ----- First HIT RN, its text modification, its CA index name, and
 its structure diagram
 FHITSEQ ----- First HIT RN, its text modification, its CA index name, its
 structure diagram, plus NTE and SEQ fields
 KWIC ----- Hit term plus 20 words on either side
 OCC ----- Number of occurrence of hit term and field in which it occurs

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All of the formats (except for SAM, SCAN, HIT, HITIND, HITRN, HITSTR, FHITSTR, HITSEQ, FHITSEQ, KWIC, and OCC) may be used with DISPLAY ACC to view a specified Accession Number.

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(FILE 'HOME' ENTERED AT 14:07:44 ON 21 JUL 2008)

FILE 'REGISTRY' ENTERED AT 14:08:05 ON 21 JUL 2008

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L3      129 S AATGAAATGCTCAGA/SQLN
L4      88 S GAATGAAATGCTCAG/SQLN
L5      144 S TGAATGAAATGCTCA/SQLN
L6      493 S L1 OR L2 OR L3 OR L4 OR L5
L7      1 S L6 AND SQL<=50
  
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FILE 'CAPLUS' ENTERED AT 14:14:59 ON 21 JUL 2008

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L9 146 S L6
L10 7 S L9 NOT PY>2000

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L10 ANSWER 1 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2000:767749 CAPLUS

DOCUMENT NUMBER: 133:318131

TITLE: Characterization and repeat analysis of the compact genome of the freshwater pufferfish *Tetraodon nigroviridis*

AUTHOR(S): Crollius, H. Roest; Jaillon, O.; Dasilva, C.; Ozouf-Costaz, C.; Fizames, C.; Fischer, C.; Bouneau, L.; Billault, A.; Quetier, F.; Saurin, W.; Bernot, A.; Weissenbach, J.

CORPORATE SOURCE: Genoscope, Evry, 91057, Fr.
SOURCE: Genome Research (2000), 10(7), 939-949

CODEN: GEREFS; ISSN: 1088-9051

PUBLISHER: Cold Spring Harbor Laboratory Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB *Tetraodon nigroviridis* is a freshwater pufferfish 20-30 million years distant from *Fugu rubripes*. The genome of both tetraodontiforms is compact, mostly because intergenic and intronic sequences are reduced in size compared to other vertebrate genomes. The previously uncharacterized *Tetraodon* genome is described here together with a detailed anal. of its repeat content and organization. The sequencing of 46 megabases of bacterial artificial chromosome (BAC) end sequences is reported, which represents a random DNA sample equivalent to 13% of the genome. The sequence and location of rRNA gene clusters, centromeric and subtelocentric satellite sequences were determined. Minisatellites and microsatellites were cataloged and notable differences were observed in comparison with microsatellites from *Fugu*. The genome contains homologies to all known families of transposable elements, including Ty3-gypsy, Ty1-copia, Line retrotransposons, DNA transposons, and retroviruses, although their overall abundance is <1%. This structural anal. is an important prerequisite to sequencing the *Tetraodon* genome. [This abstract record is one of 10 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

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269821-42-3 269821-43-4 269821-44-5 269821-45-6 269821-46-7
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269822-02-8	269822-03-9	269822-04-0	269822-05-1	269822-06-2
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269822-37-9	269822-38-0	269822-39-1	269822-40-4	269822-41-5
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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(nucleotide sequence; characterization and repeat anal. of the compact genome of the freshwater pufferfish *Tetraodon nigroviridis*)

L10 ANSWER 2 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2000:767717 CAPLUS

DOCUMENT NUMBER: 133:318128

TITLE: Characterization and repeat analysis of the compact genome of the freshwater pufferfish *Tetraodon nigroviridis*

AUTHOR(S): Crollius, H. Roest; Jaillon, O.; Dasilva, C.; Ozouf-Costaz, C.; Fizames, C.; Fischer, C.; Bouneau, L.; Billault, A.; Quetier, F.; Saurin, W.; Bernot, A.; Weissenbach, J.

CORPORATE SOURCE: Genoscope, Evry, 91057, Fr.

SOURCE: Genome Research (2000), 10(7), 939-949

CODEN: GEREFS; ISSN: 1088-9051

PUBLISHER: Cold Spring Harbor Laboratory Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB *Tetraodon nigroviridis* is a freshwater pufferfish 20-30 million years distant from *Fugu rubripes*. The genome of both tetraodontiforms is compact, mostly because intergenic and intronic sequences are reduced in size compared to other vertebrate genomes. The previously uncharacterized *Tetraodon* genome is described here together with a detailed anal. of its repeat content and organization. The sequencing of 46 megabases of bacterial artificial chromosome (BAC) end sequences is reported, which represents a random DNA sample equivalent to 13% of the genome. The sequence and location of rRNA gene clusters, centromeric and subtelocentric satellite sequences were determined. Minisatellites and microsatellites were cataloged and notable differences were observed in comparison with microsatellites from *Fugu*. The genome contains homologies to all known families of transposable elements, including Ty3-gypsy, Ty1-copia, Line

retrotransposons, DNA transposons, and retroviruses, although their overall abundance is <1%. This structural anal. is an important prerequisite to sequencing the Tetraodon genome. [This abstract record is one of 10 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(nucleotide sequence; characterization and repeat anal. of the compact genome of the freshwater pufferfish *Tetraodon nigroviridis*)

TITLE: A sea urchin genome project: sequence scan, virtual map, and additional resources

AUTHOR(S): Cameron, R. Andrew; Mahairas, Gregory; Rast, Jonathan P.; Martinez, Pedro; Biondi, Ted R.; Swartzell, Steven; Wallace, James C.; Poustka, Albert J.; Livingston, Brian T.; Wray, Gregory A.; Etensohn, Charles A.; Lehrach, Hans; Britten, Roy J.; Davidson, Eric H.; Hood, Leroy

CORPORATE SOURCE: Stowers Inst. Med. Res., Kansas City, MO, 64110, USA

SOURCE: Proceedings of the National Academy of Sciences of the United States of America (2000), 97(17), 9514-9518
CODEN: PNASA6; ISSN: 0027-8424

PUBLISHER: National Academy of Sciences

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Results of a first-stage Sea Urchin Genome Project are summarized. The species chosen was *Strongylocentrotus purpuratus*, a research model of major importance in developmental and mol. biol. A virtual map of the genome was constructed by sequencing the ends of 76,020 bacterial artificial chromosome (BAC) recombinants (average length, 125 kb). The BAC-end sequence tag connectors (STCs) occur an average of 10 kb apart, and, together with restriction digest patterns recorded for the same BAC clones, they provide immediate access to contigs of several hundred kilobases surrounding any gene of interest. The STCs survey >5% of the genome and provide the estimate that this genome contains \approx 27,350 protein-coding genes. The frequency distribution and canonical sequences of all middle and highly repetitive sequence families in the genome were obtained from the STCs as well. The 500-kb Hox gene complex of this species is being sequenced in its entirety. In addition, arrayed cDNA libraries of >105 clones each were constructed from every major stage of embryogenesis, several individual cell types, and adult tissues and are available to the community. The accumulated STC data (AZ135866-AZ211804) and an expanding expressed sequence tag database (at present including >12,000 sequences) have been reported to GenBank and are accessible on public web sites. [This abstract record is one of 19 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(nucleotide sequence; sea urchin genome project including sequence
scan, virtual map, and addnl. resources)

L10 ANSWER 4 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2000:366621 CAPLUS

DOCUMENT NUMBER: 132:344010

TITLE: The DNA sequence of human chromosome 21

AUTHOR(S): Hattori, M.; Fujiyama, A.; Taylor, T. D.; Watanabe, H.; Yada, T.; Park, H.-S.; Toyoda, A.; Ishii, K.; Totoki, Y.; Choi, D.-K.; Soeda, E.; Ohki, M.; Takagi, T.; Sakaki, Y.; Taudien, S.; Blechschmidt, K.; Polley, A.; Menzel, U.; Delabar, J.; Kumpf, K.; Lehmann, R.; Patterson, D.; Reichwald, K.; Rump, A.; Schillhabel, M.; Schudy, A.; Zimmermann, W.; Rosenthal, A.; Kudoh, J.; Shibuya, K.; Kawasaki, K.; Asakawa, S.; Shintani, A.; Sasaki, T.; Nagamine, K.; Mitsuyma, S.; Antonarakis, S. E.; Minoshima, S.; Shimizu, N.; Nordtsiek, G.; Hornischer, K.; Brandt, P.; Scharfe, M.; Schon, O.; Desario, A.; Reichelt, J.; Kauer, G.; Blocker, H.; Ramser, J.; Beck, A.; Klages, S.; Hennig, S.; Riesselmann, L.; Dagand, E.; Haaf, T.; Wehrmeyer, S.; Borzym, K.; Gardiner, K.; Nizetic, D.; Francis, F.; Lehrach, H.; Reinhardt, R.; Yaspo, M.-L.

CORPORATE SOURCE: Genomic Sciences Center, RIKEN, Sagami-hara, 228-8555, Japan

SOURCE: Nature (London) (2000), 405(6784), 311-319

CODEN: NATUAS; ISSN: 0028-0836

PUBLISHER: Nature Publishing Group

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Chromosome 21 is the smallest human autosome. An extra copy of chromosome 21 causes Down syndrome, the most frequent genetic cause of significant mental retardation, which affects up to 1 in 700 live births. Several anonymous loci for monogenic disorders and predispositions for common complex disorders have also been mapped to this chromosome, and loss of heterozygosity has been observed in regions associated with solid tumors. This report provides the sequence and gene catalog of the long arm of

chromosome 21. At least 33,546,361 base pairs (bp) of DNA have been sequenced with very high accuracy, the largest contig being 25,491,867 bp. Only 3 small clone gaps and 7 sequencing gaps remain, comprising .apprx.100 kilobases. Thus, 99.7% coverage of 21q was achieved. About 281,116 bp were also sequenced from the short arm. The structural features identified include duplications that are probably involved in chromosomal abnormalities and repeat structures in the telomeric and pericentromeric regions. Anal. of the chromosome revealed 127 known genes, 98 predicted genes and 59 pseudogenes. The sequences are deposited in the GenBank database, and addnl. information can be found from the home pages of the participating centers of the chromosome 21 sequencing consortium.

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 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (nucleotide sequence; DNA sequence of human chromosome 21)

L10 ANSWER 5 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2000:246921 CAPLUS

DOCUMENT NUMBER: 132:275067

TITLE:

AUTHOR(S):

The genome sequence of *Drosophila melanogaster*
 Adams, Mark D.; Celniker, Susan E.; Holt, Robert A.;
 Evans, Cheryl A.; Gocayne, Jeannine D.; Amanatides,
 Peter G.; Scherer, Steven E.; Li, Peter W.; Hoskins,
 Roger A.; Galle, Richard F.; George, Reed A.; Lewis,
 Suzanna E.; Richards, Stephen; Ashburner, Michael;
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 Jennifer R.; Yandell, Mark D.; Zhang, Qing; Chen, Lin
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 Kenneth H.; Doyle, Clare; Baxter, Evan G.; Helt,
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 Richard W.; Basu, Anand; Baxendale, James;
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 Kristina; Doup, Lisa E.; Downes, Michael; Dugan-Rocha,
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 Saul; Kulp, David; Lai, Zhongwu; Lasko, Paul; Lei,
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 Nelson, David R.; Nelson, Keith A.; Nixon, Katherine;
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Remington, Karin; Saunders, Robert D. C.; Scheeler, Frederick; Shen, Hua; Shue, Bixiang Christopher; Siden-Kiamos, Inga; Simpson, Michael; Skupski, Marian P.; Smith, Tom; Spier, Eugene; Spradling, Allan C.; Stapleton, Mark; Strong, Renee; Sun, Eric; Svirskas, Robert; Tector, Cyndee; Turner, Russell; Venter, Eli; Wang, Aihui H.; Wang, Xin; Wang, Zhen-Yuan; Wassarman, David A.; Weinstock, George M.; Weissenbach, Jean; Williams, Sherita M.; Woodage, Trevor; Worley, Kim C.; Wu, David; Yang, Song; Yao, Q. Alison; Ye, Jane; Yeh, Ru-Fang; Zaveri, Jayshree S.; Zhan, Ming; Zhang, Guangren; Zhao, Qi; Zheng, Liansheng; Zheng, Xiangqun H.; Zhong, Fei N.; Zhong, Wenyan; Zhou, Xiaojun; Zhu, Shiaooping; Zhu, Xiaohong; Smith, Hamilton O.; Gibbs, Richard A.; Myers, Eugene W.; Rubin, Gerald M.; Venter, J. Craig

CORPORATE SOURCE: Celera Genomics, Rockville, MD, 20850, USA
SOURCE: Science (Washington, D. C.) (2000), 287(5461), 2185-2195

CODEN: SCIEAS; ISSN: 0036-8075
PUBLISHER: American Association for the Advancement of Science
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The fly *Drosophila melanogaster* is one of the most intensively studied organisms in biol. and serves as a model system for the investigation of many developmental and cellular processes common to higher eukaryotes, including humans. The nucleotide sequence was determined of nearly all of the .apprx.120-megabase euchromatic portion of the *Drosophila* genome using a whole-genome shotgun sequencing strategy supported by extensive clone-based sequence and a high-quality bacterial artificial chromosome phys. map. Efforts are under way to close the remaining gaps; however, the sequence is of sufficient accuracy and contiguity to be declared substantially complete and to support an initial anal. of genome structure and preliminary gene annotation and interpretation. The genome encodes .apprx.13,600 genes, somewhat fewer than the smaller *Caenorhabditis elegans* genome, but with comparable functional diversity. Access to supporting information on each gene is available through FlyBase at <http://flybase.bio.indiana.edu> and through Celera at www.celera.com; the sequences are deposited in GenBank with Accession Nos. AE002566-AE003403. [This abstract record is one of 4 records for this document necessitated by the large number of index entries required to fully index the document and publication system restraints.]

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)

(nucleotide sequence; genome sequence of *Drosophila melanogaster*)

L10 ANSWER 6 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2000:246831 CAPLUS

DOCUMENT NUMBER: 132:275066

TITLE: The genome sequence of *Drosophila melanogaster*

AUTHOR(S): Adams, Mark D.; Celniker, Susan E.; Holt, Robert A.; Evans, Cheryl A.; Gocayne, Jeannine D.; Amanatides, Peter G.; Scherer, Steven E.; Li, Peter W.; Hoskins, Roger A.; Galle, Richard F.; George, Reed A.; Lewis, Suzanna E.; Richards, Stephen; Ashburner, Michael; Henderson, Scott N.; Sutton, Granger G.; Wortman, Jennifer R.; Yandell, Mark D.; Zhang, Qing; Chen, Lin X.; Brandon, Rhonda C.; Rogers, Yu-Hui C.; Blazej, Robert G.; Champe, Mark; Pfeiffer, Barret D.; Wan, Kenneth H.; Doyle, Clare; Baxter, Evan G.; Helt, Gregg; Nelson, Catherine R.; Miklos, George L. Gabor; Abril, Josep F.; Agbayani, Anna; An, Hui-Jin; Andrews-Pfannkoch, Cynthia; Baldwin, Danita; Ballew, Richard M.; Basu, Anand; Baxendale, James; Bayraktaroglu, Leyla; Beasley, Ellen M.; Beeson, Karen Y.; Benos, P. V.; Berman, Benjamin P.; Bhandari, Deepali; Bolshakov, Slava; Borkova, Dana; Botchan, Michael R.; Bouck, John; Brokstein, Peter; Brottier, Philippe; Burtis, Kenneth C.; Busam, Dana A.; Butler, Heather; Cadieu, Edouard; Center, Angela; Chandra, Ishwar; Cherry, J. Michael; Cawley, Simon; Dahlke, Carl; Davenport, Lionel B.; Davies, Peter; De Pablos, Beatriz De; Delcher, Arthur; Deng, Zuoming; Mays, Anne Deslattes; Dew, Ian; Dietz, Suzanne M.; Dodson, Kristina; Doup, Lisa E.; Downes, Michael; Dugan-Rocha, Shannon; Dunkov, Boris C.; Dunn, Patrick; Durbin,

Kenneth J.; Evangelista, Carlos C.; Ferraz, Concepcion; Ferriera, Steven; Fleischmann, Wolfgang; Foster, Carl; Gabrielian, Andrei E.; Garg, Neha S.; Gelbart, William M.; Glasser, Ken; Glodek, Anna; Gong, Fangcheng; Gorrell, J. Harley; Gu, Zhiping; Guan, Ping; Harris, Michael; Harris, Nomi L.; Harvey, Damon; Heiman, Thomas J.; Hernandez, Judith R.; Houck, Jarrett; Hostin, Damon; Houston, Kathryn A.; Howland, Timothy J.; Wei, Ming-Hui; Ibegwam, Chinyere; Jalali, Mena; Kalush, Francis; Karpen, Gary H.; Ke, Zhaoxi; Kennison, James A.; Ketchum, Karen A.; Kimmel, Bruce E.; Kodira, Chinnappa D.; Kraft, Cheryl; Kravitz, Saul; Kulp, David; Lai, Zhongwu; Lasko, Paul; Lei, Yiding; Levitsky, Alexander A.; Li, Jiayin; Li, Zhenya; Liang, Yong; Lin, Xiaoying; Liu, Xiangjun; Mattei, Bettina; McIntosh, Tina C.; McLeod, Michael P.; McPherson, Duncan; Merkulov, Gennady; Milshina, Natalia V.; Mobarrey, Clark; Morris, Joe; Moshrefi, Ali; Mount, Stephen M.; Moy, Mee; Murphy, Brian; Murphy, Lee; Muzny, Donna M.; Nelson, David L.; Nelson, David R.; Nelson, Keith A.; Nixon, Katherine; Nusskern, Deborah R.; Pacleb, Joanne M.; Palazzolo, Michael; Pittman, Gjang S.; Pan, Sue; Pollard, John; Puri, Vinita; Reese, Martin G.; Reinert, Knut; Remington, Karin; Saunders, Robert D. C.; Scheeler, Frederick; Shen, Hua; Shue, Bixiang Christopher; Siden-Kiamos, Inga; Simpson, Michael; Skupski, Marian P.; Smith, Tom; Spier, Eugene; Spradling, Allan C.; Stapleton, Mark; Strong, Renee; Sun, Eric; Svirskas, Robert; Tector, Cyndee; Turner, Russell; Venter, Eli; Wang, Aihui H.; Wang, Xin; Wang, Zhen-Yuan; Wassarman, David A.; Weinstock, George M.; Weissbach, Jean; Williams, Sherita M.; Woodage, Trevor; Worley, Kim C.; Wu, David; Yang, Song; Yao, Q. Alison; Ye, Jane; Yeh, Ru-Fang; Zaveri, Jayshree S.; Zhan, Ming; Zhang, Guangren; Zhao, Qi; Zheng, Liansheng; Zheng, Xiangqun H.; Zhong, Fei N.; Zhong, Wenyan; Zhou, Xiaojun; Zhu, Shiaoqing; Zhu, Xiaohong; Smith, Hamilton O.; Gibbs, Richard A.; Myers, Eugene W.; Rubin, Gerald M.; Venter, J. Craig

Celera Genomics, Rockville, MD, 20850, USA
 SOURCE: Science (Washington, D. C.) (2000), 287(5461), 2185-2195
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PUBLISHER: American Association for the Advancement of Science
 DOCUMENT TYPE: Journal
 LANGUAGE: English

AB The fly *Drosophila melanogaster* is one of the most intensively studied organisms in biol. and serves as a model system for the investigation of many developmental and cellular processes common to higher eukaryotes, including humans. The nucleotide sequence was determined of nearly all of the .apprx.120-megabase euchromatic portion of the *Drosophila* genome using a whole-genome shotgun sequencing strategy supported by extensive clone-based sequence and a high-quality bacterial artificial chromosome phys. map. Efforts are under way to close the remaining gaps; however, the sequence is of sufficient accuracy and contiguity to be declared substantially complete and to support an initial anal. of genome structure and preliminary gene annotation and interpretation. The genome encodes .apprx.13,600 genes, somewhat fewer than the smaller *Caenorhabditis elegans* genome, but with comparable functional diversity. Access to supporting information on each gene is available through FlyBase at <http://flybase.bio.indiana.edu> and through Celera at www.celera.com; the

sequences are deposited in GenBank with Accession Nos. AE002566-AE003403.
[This abstract record is one of 4 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints].

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260227-62-1

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(nucleotide sequence; genome sequence of *Drosophila melanogaster*)

L10 ANSWER 7 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2000:47778 CAPLUS

DOCUMENT NUMBER: 132:118215

TITLE: Generation and analysis of 25 Mb of genomic DNA from

the pufferfish *Fugu rubripes* by sequence scanning
Elgar, Greg; Clark, Melody S.; Meek, Stephen; Smith,
Sarah; Warner, Sarah; Edwards, Yvonne J. K.;
Bouchireb, Nassima; Cottage, Amanda; Yeo, Giles S. H.;
Umrana, Yagnesh; Williams, Gary; Brenner, Sydney

CORPORATE SOURCE: UK Human Genome Mapping Project (HGMP) Resource
Centre, Hinxton, Cambridge, CB10 1SB, UK

SOURCE: Genome Research (1999), 9(10), 960-971

CODEN: GEREFS; ISSN: 1088-9051
Cold Spring Harbor Laboratory Press
Journal
English

PUBLISHER:
DOCUMENT TYPE:
LANGUAGE:

AB Over 50,000 shotgun clones were generated and analyzed from 1059 Fugu cosmid clones. All sequences have been minimally edited and searched against protein and DNA databases. These data are all displayed on a searchable, publicly available web site at <http://fugu.hgmp.mrc.ac.uk/>. With an average of 50 reads per cosmid, this is virtually nonredundant sequence skimming, covering 30%-50% of each clone. This essentially random data set covers nearly 25 Mb (>6%) of the Fugu genome and forms the basis of a series of whole genome analyses which address questions regarding gene d. and distribution in the Fugu genome and the similarity between Fugu and mammalian genes. The Fugu genome, with 8-fold less DNA but a similar gene repertoire, is ideally suited to this type of study because most cosmids contain more than one identifiable gene. General features of the genome are also discussed. Some estimation was made of the syntenic relationship between mammals and Fugu and the efficacy of ORF prediction from short, unedited Fugu genomic sequences studied. Comparative DNA sequence analyses are an essential tool in the functional interpretation of complex vertebrate genomes. This project highlights the utility of using the Fugu genome in this kind of study. [This abstract record is the third of 10 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

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197543-54-7,	GenBank	AL005256	197543-55-8,	GenBank	AL005257
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197543-64-9,	GenBank	AL005266	197543-65-0,	GenBank	AL005267
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197543-68-3,	GenBank	AL005270	197543-69-4,	GenBank	AL005271
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197544-10-8,	GenBank	AL005324	197544-11-9,	GenBank	AL005325
197544-12-0,	GenBank	AL005326	197544-13-1,	GenBank	AL005327
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197544-16-4,	GenBank	AL005330	197544-17-5,	GenBank	AL005331
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197544-22-2,	GenBank	AL005336	197544-23-3,	GenBank	AL005337
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197544-32-4,	GenBank	AL005346	197544-33-5,	GenBank	AL005347
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197544-36-8,	GenBank	AL005350	197544-37-9,	GenBank	AL005351
197544-38-0,	GenBank	AL005352	197544-39-1,	GenBank	AL005353
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197544-42-6,	GenBank	AL005356	197544-43-7,	GenBank	AL005357
197544-44-8,	GenBank	AL005358	197544-45-9,	GenBank	AL005359
197544-46-0,	GenBank	AL005360	197544-47-1,	GenBank	AL005361
197544-48-2,	GenBank	AL005362	197544-49-3,	GenBank	AL005363
197544-50-6,	GenBank	AL005364	197544-51-7,	GenBank	AL005365
197544-52-8,	GenBank	AL005366	197544-53-9,	GenBank	AL005367
197544-54-0,	GenBank	AL005368	197544-55-1,	GenBank	AL005369
197544-56-2,	GenBank	AL005370	197544-57-3,	GenBank	AL005444
197544-58-4,	GenBank	AL005445	197544-59-5,	GenBank	AL005446
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197544-62-0,	GenBank	AL005449	197544-63-1,	GenBank	AL005450
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197544-66-4,	GenBank	AL005373	197544-67-5,	GenBank	AL005374
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197544-94-8, GenBank AL005401	197544-95-9, GenBank AL005402
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197545-08-7, GenBank AL005415	

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(nucleotide sequence; generation and anal. of 25 Mb of genomic DNA from the pufferfish *Fugu rubripes* by sequence scanning)

=> file reg

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
54.53	217.41

FULL ESTIMATED COST

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

SINCE FILE	TOTAL
ENTRY	SESSION
-12.00	-12.00

CA SUBSCRIBER PRICE

FILE 'REGISTRY' ENTERED AT 14:22:49 ON 21 JUL 2008

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<http://www.cas.org/support/stngen/stdoc/properties.html>

=> s (269821-23-0 or 269536-84-7 or 271680-31-0 or 264819-97-8 or 260229-12-7 or 260226-80-0 or 197543-85-4)/rn


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1 269821-23-0/RN
1 269536-84-7/RN
1 271680-31-0/RN
1 264819-97-8/RN
1 260229-12-7/RN
1 260226-80-0/RN
1 197543-85-4/RN
L11 7 (269821-23-0 OR 269536-84-7 OR 271680-31-0 OR 264819-97-8 OR
260229-12-7 OR 260226-80-0 OR 197543-85-4)/RN
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=> d his

(FILE 'HOME' ENTERED AT 14:07:44 ON 21 JUL 2008)

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FILE 'REGISTRY' ENTERED AT 14:08:05 ON 21 JUL 2008
L1 134 S TGAAATGCTCAGATT/SQSN
L2 141 S ATGAAATGCTCAGAT/SQSN
L3 129 S AATGAAATGCTCAGA/SQSN
L4 88 S GAATGAAATGCTCAG/SQSN
L5 144 S TGAATGAAATGCTCA/SQSN
L6 493 S L1 OR L2 OR L3 OR L4 OR L5
L7 1 S L6 AND SQL<=50
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FILE 'CAPLUS' ENTERED AT 14:14:59 ON 21 JUL 2008
L8 1 S L7
L9 146 S L6
L10 7 S L9 NOT PY>2000
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FILE 'REGISTRY' ENTERED AT 14:22:49 ON 21 JUL 2008
L11 7 S (269821-23-0 OR 269536-84-7 OR 271680-31-0 OR 264819-97-8 OR
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=> s l11 and l6
L12 7 L11 AND L6

=> d reg sql seq 1-7
1 RN 271680-31-0 REGISTRY

L12 ANSWER 1 OF 7 REGISTRY COPYRIGHT 2008 ACS on STN
SQL 811

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SEQ 1 gagcgcttcc gcgacattct ttttgtcct ctgtgacaaa tactcagact
51 gttttgtgtg aaatgctcag attagatttg ctgaattctg atattctttc
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101 atatgtttct catttgtttc cagttaacat tttgtgtggt cttgtcatg
151 tatgttgaat gttatgttga ttattgtccc ttntcacca tttttgttcc
201 tttttcacca tttttgtttt ctcttcacaa tgaggttatt actttgtttc
251 agaattgatt taaggggaaa aaaggaaaac gtcttataaa gtgagaaaaa
301 gaatttgtgt acatgtatat caatttattt aaacaatat gatgtccga
351 tgtattgtat aaagagcatt caatttaaat gttttcattg tttttaagtt
401 gataataaaa cagaaaaaaa tacaaacatg acaaaaaaat gatattggct
451 taatgacctt gttgaagata tgccctgcag tactttcttg gcttgtatgt
501 ttagtgtggt catacgata gtttcttttt ttacgcctt tgtgaacatg
551 tactacatct actattacga ttactactac tacttctact gttattgttt
601 cttgggaaatg ataatgcaat attttttatt gacaattcca atggagacat
651 aaaaagagaaa tgttgggtggc ttgaacctat taaataaaa cacaacaacat
701 gtaaaacaaa tattactatt ggcgtggata attcacagaa acactggacc
751 cnnnctatcc tctnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
801 nnnnnnnnnn a
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HITS AT: 59-73
2 RN 269821-23-0 REGISTRY

L12 ANSWER 2 OF 7 REGISTRY COPYRIGHT 2008 ACS on STN

SQL 1101

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SEQ      1 aaanaacttt gaaaaacaaa cattaacaaa actacnaacg aaccttcgatg
51 aactggantc atgcagtgaa attttgactc aaaagtncaa aananaggct
101 ctttatctgc ctctccgca gagcttctct tcacttttat cttttctctc
151 cattntnca ggtgtacttc gtttatgacg aagaggtgga agaggaggag
201 aaggatgaac ctctcccat agaaccagtc aaaccagtca acgacaggcc
251 tcacaagttc aaggaccact actgcaagaa gccaaaaatc tgcgacgtct
301 gcgcgcgat gatcgtgtgt acgtgcgcgg tgcgtgtgct gaccgctggc
351 agaggtgggt cagaggcgac ctgttcacgt gtgtccgctc ttgtctggat
401 ttgcctcttc agtgaacaac aagtttgcgc tcaggtgcaa gaactgcaaa
451 accagcatcc accaccagt ccagtcctac gtggagttcc agagtgctt
501 cggcaaaatt gtgagtgtca ctaaaagcga cggttgatcc aagccgcgcg
551 aggccttagc cngtgcctct ctctccggtt agcctccagg cttcaggaga
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901 caaagatgtg acaaatgcac tagtgtaatt attttactca tgaatgctc
=====
951 agatgatgat gatgatggag gatgacgagt cgcagcccaa aaccggacga
=====
1001 cgacgaagga agccaaggag gtaaaagcaa tcgggccana gctgagggcg
1051 ctcacggcga caaagaggaa ctgtttctcg acagaaatgc cctctctnt
1101 t
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HITS AT: 940-954

3 RN 269536-84-7 REGISTRY

L12 ANSWER 3 OF 7 REGISTRY COPYRIGHT 2008 ACS on STN

SQL 1018

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SEQ      1 tnnagtaanc aatnattaac aaaactacta acgaaccttc atgaactgnt
51 tcatgcagtg aaattttgac tcaaaantgc aaaaanagagg ctctttatct
101 gcctctccgt cagagcttct ctctactttt atctttcttc ctcatttctg
151 caggtgtact tcgtttatga cgaagagggt gaagaggagg agaaggatga
201 acctctcccc atagaaccag tcaaacaggt caacgacagg cctcacaagt
251 tcaaggacca ctactgcaag aagccaaaat tctgcgact ctgcgcgcgc
301 atgatcgtgt gtacgtgcgc gacgcgtgtg ctgagcgcgt gcagaggtgg
351 tcgacaggcg acctgttcac gtgtgtccgc tctgttctgg atttgcctct
401 ttagtgaaca acaagtttgc gctcaggtgc aagaactgca aaaccagcat
451 ccaccaccag tgccagtctc acgtggagtg ccagaggtgc ttggcgaaaa
501 ttgtgagtg cactaaaagc acggttgat ccaagccgcc gcaggcttta
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901 gatgtgacaa atgcactagt gtaattattt tactcatgaa atgtcagat
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951 gatganatgg atggnnggat angagtcgca gccnaaacgg gacgacgaga
1001 aggagncnaa gngggtaa
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HITS AT: 936-950

4 RN 264819-97-8 REGISTRY

L12 ANSWER 4 OF 7 REGISTRY COPYRIGHT 2008 ACS on STN

SQL 340000

SEQ 1 aagaagatga gcagactcac ggaccatga gtccacagca agcagcccat

51	tcgagtacct	gggactgcag	gaggcagggg	aagagaccga	atagctagaa
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151	ccaaaacacac	cacacataacc	ctaaagctta	tcaaattaca	gaaaaccagg
201	gataaagaga	aaaaaacaaa	agcagccgca	gaatacatat	atgatgacta
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451	gagacgcagc	tctgacctga	gtggggctat	gatgtgccgg	gtggtgcagt
501	ttggccaaggt	gcagcaggcc	aaggcctgag	agcaggaagc	ccggggcagg
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901	gaaggggtga	ctgggcacgg	agaggcaaga	cacggatagc	tggagatacc
951	gtgtgggggc	cacacataat	tgacgtgca	catacaatca	ccctcccaat
1001	atgaagcaca	aaacagggct	caacaaatct	aaagagaggg	aagtgcagca
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1101	acaaaatctg	gaggaaaacc	ctaaatgttt	ggaaattaaa	ccatctttcc
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1201	tatcacgtca	acataatatt	ggtacaggaa	gaaacacaga	aagctctcct
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3251	tcaaggtacc	agcaagaagg	cagctgcgcc	atccactgag	acacagaaaac
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L1 0 WO0120025/PN
(WO120025/PN)

=> s WO 0120025/pn
L2 0 WO 0120025/PN
(WO120025/PN)

=> s WO 01/20025/pn
L3 1 WO 01/20025/PN
(WO2001020025/PN)

=> d ibib

L3 ANSWER 1 OF 1 PCTFULL COPYRIGHT 2008 Univention on STN
ACCESSION NUMBER: 2001020025 PCTFULL ED 20020820
TITLE (ENGLISH): POLYMORPHISMS IN THE HUMAN CYP3A4 AND CYP3A7 GENES AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
TITLE (FRENCH): POLYMORPHISMES DANS LES GENES HUMAINS CYP3A4 ET CYP3A7
ET LEURS APPLICATIONS EN MATIERE DE DIAGNOSTIC ET DE
THERAPIE
INVENTOR(S): WOJNOWSKI, Leszek;
EISELT, Regina
PATENT ASSIGNEE(S): EPIDAUROS BIOTECHNOLOGIE AG;
WOJNOWSKI, Leszek;
EISELT, Regina
DOCUMENT TYPE: Patent
PATENT INFORMATION: NUMBER KIND DATE

DESIGNATED STATES

W:

WO 2001020025

A2 20010322

AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU
 CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN
 IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK
 MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM
 TR TT TZ UA UG US UZ VN YU ZA ZW GH GM KE LS MW MZ SD
 SL SZ TZ UG ZW AM AZ BY KG KZ MD RU TJ TM AT BE CH CY
 DE DK ES FI FR GB GR IE IT LU MC NL PT SE BF BJ CF CG
 CI CM GA GN GW ML MR NE SN TD TG
 EP 1999-991 18 120.7 19990910
 WO 2000-EP8570 A 20000901

PRIORITY INFO.:

APPLICATION INFO.:

=> d his

(FILE 'HOME' ENTERED AT 12:14:47 ON 14 NOV 2008)

FILE 'PCTFULL' ENTERED AT 12:15:34 ON 14 NOV 2008

L1 0 S WO0120025/PN
 L2 0 S WO 0120025/PN
 L3 1 S WO 01/20025/PN

=> s l3 and (corresponding position)

596809 CORRESPONDING
 14 CORRESPONDINGS
 596811 CORRESPONDING
 (CORRESPONDING OR CORRESPONDINGS)
 611584 POSITION
 270164 POSITIONS
 653128 POSITION
 (POSITION OR POSITIONS)
 10079 CORRESPONDING POSITION
 (CORRESPONDING(W)POSITION)

L4 1 L3 AND (CORRESPONDING POSITION)

=> d ibib kwic

L4 ANSWER 1 OF 1 PCTFULL COPYRIGHT 2008 Univentio on STN
 2001020025 PCTFULL ED 20020820
 ACCESSION NUMBER:
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 INVENTOR(S): WOJNOWSKI, Leszek;
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 EISELT, Regina
 DOCUMENT TYPE: Patent
 PATENT INFORMATION:

NUMBER	KIND	DATE
WO 2001020025	A2	20010322

DESIGNATED STATES

W:

AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU
 CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN
 IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK
 MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM
 TR TT TZ UA UG US UZ VN YU ZA ZW GH GM KE LS MW MZ SD

SL SZ TZ UG ZW AM AZ BY KG KZ MD RU TJ TM AT BE CH CY
 DE DK ES FI FR GB GR IE IT LU MC NL PT SE BF BJ CF CG
 CI CM GA GN GW ML MR NE SN TD TG
 EP 1999-991 18 120.7 19990910
 APPLICATION INFO.: WO 2000-EP8570 A 20000901
 PI WO 2001020025 A2 20010322

DETD . . . may vary due to deletions or additional nucleotides or amino acids elsewhere in the gene or the polypeptide. Thus, under a corresponding position in accordance with the present invention it is to be understood that nucleotides or amino acids may differ in the indicated. . . nucleotides or amino acids which may be exchanged, deleted or comprise additional nucleotides or amino acids are also comprised by the term corresponding position . Said nucleotides or amino acids may for instance together with their neighbors form sequences which may be involved in the regulation of. . .

=>

---Logging off of STN---

=>

Executing the logoff script...

=> LOG Y

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	8.51	8.72

STN INTERNATIONAL LOGOFF AT 12:17:21 ON 14 NOV 2008

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:SSSPTA1642BJF

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * Welcome to STN International * * * * *

NEWS	1	Web Page for STN Seminar Schedule - N. America
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NEWS	3 JUL 28	EPFULL enhanced with additional legal status information from the epoline Register

NEWS 4 JUL 28 IFICDB, IFIPAT, and IFIUDB reloaded with enhancements
 NEWS 5 JUL 28 STN Viewer performance improved
 NEWS 6 AUG 01 INPADOCDB and INPAFAMDB coverage enhanced
 NEWS 7 AUG 13 CA/CAPlus enhanced with printed Chemical Abstracts
 page images from 1967-1998
 NEWS 8 AUG 15 CAOLD to be discontinued on December 31, 2008
 NEWS 9 AUG 15 CAPlus currency for Korean patents enhanced
 NEWS 10 AUG 27 CAS definition of basic patents expanded to ensure
 comprehensive access to substance and sequence
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 to be discontinued
 NEWS 12 SEP 25 CA/CAPlus current-awareness alert options enhanced
 to accommodate supplemental CAS indexing of
 exemplified prophetic substances
 NEWS 13 SEP 26 WPIDS, WPINDEX, and WPIX coverage of Chinese and
 and Korean patents enhanced
 NEWS 14 SEP 29 IFICLS enhanced with new super search field
 NEWS 15 SEP 29 EMBASE and EMBAL enhanced with new search and
 display fields
 NEWS 16 SEP 30 CAS patent coverage enhanced to include exemplified
 prophetic substances identified in new Japanese-
 language patents
 NEWS 17 OCT 07 EPFULL enhanced with full implementation of EPC2000
 NEWS 18 OCT 07 Multiple databases enhanced for more flexible patent
 number searching
 NEWS 19 OCT 22 Current-awareness alert (SDI) setup and editing
 enhanced
 NEWS 20 OCT 22 WPIDS, WPINDEX, and WPIX enhanced with Canadian PCT
 Applications
 NEWS 21 OCT 24 CHEMLIST enhanced with intermediate list of
 pre-registered REACH substances
 NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,
 AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.
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* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 12:34:32 ON 14 NOV 2008

=> file reg		
COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	0.21	0.21

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DICTIONARY FILE UPDATES: 13 NOV 2008 HIGHEST RN 1072687-23-0

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<http://www.cas.org/support/stngen/stdoc/properties.html>

=> s EML/SQSP
L1 206279 EML/SQSP

	SINCE FILE	TOTAL
	ENTRY	SESSION
=> file caplus		
COST IN U.S. DOLLARS		
FULL ESTIMATED COST	30.86	31.07

FILE 'CAPLUS' ENTERED AT 12:35:12 ON 14 NOV 2008
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FILE LAST UPDATED: 13 Nov 2008 (20081113/ED)

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=> s l1
<-----User Break----->

SEARCH ENDED BY USER

=> file reg

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	0.48	31.55

FILE 'REGISTRY' ENTERED AT 12:35:45 ON 14 NOV 2008
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STRUCTURE FILE UPDATES: 13 NOV 2008 HIGHEST RN 1072687-23-0
 DICTIONARY FILE UPDATES: 13 NOV 2008 HIGHEST RN 1072687-23-0

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=> s l1 and sql<=100
      10694085 SQL<=100
L2      7769 L1 AND SQL<=100
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=> file caplus	ENTRY	SESSION
COST IN U.S. DOLLARS	5.61	37.16
FULL ESTIMATED COST		

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=> s l2

L3 2444 L2

=> s l3 not py>1999

10288553 PY>1999

L4 354 L3 NOT PY>1999

=> d hitseq

L4 ANSWER 1 OF 354 CAPLUS COPYRIGHT 2008 ACS on STN

IT 489078-58-2

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)

(amino acid sequence; genomic sequence comparison of two unrelated
isolates of the human gastric pathogen *Helicobacter pylori*)

RN 489078-58-2 CAPLUS

CN Protein (*Helicobacter pylori* strain J99 gene jhp1419) (9CI) (CA INDEX
NAME)

SEQ 1 MFEKIRKILA DIEDSQNEIE MLLKLANLSL GDFIEIKRGS MDMPKGVNEA

51 FFTQLSEEEV RLKELINALN KIKKGLLVF

=>

---Logging off of STN---

=>

Executing the logoff script...

=> LOG Y

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

FULL ESTIMATED COST

8.44

45.60

STN INTERNATIONAL LOGOFF AT 12:37:24 ON 14 NOV 2008

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Welcome to STN International! Enter x:x

LOGINID:SSSPTA1642BJF

PASSWORD:

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NEWS 9 AUG 15 CAPLUS currency for Korean patents enhanced
NEWS 10 AUG 27 CAS definition of basic patents expanded to ensure
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NEWS 11 SEP 18 Support for STN Express, Versions 6.01 and earlier,
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NEWS 12 SEP 25 CA/CAPLUS current-awareness alert options enhanced
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exemplified prophetic substances
NEWS 13 SEP 26 WPIDS, WPINDEX, and WPIX coverage of Chinese and
and Korean patents enhanced
NEWS 14 SEP 29 IFICLS enhanced with new super search field
NEWS 15 SEP 29 EMBASE and EMBAL enhanced with new search and
display fields
NEWS 16 SEP 30 CAS patent coverage enhanced to include exemplified
prophetic substances identified in new Japanese-
language patents
NEWS 17 OCT 07 EFFULL enhanced with full implementation of EPC2000
NEWS 18 OCT 07 Multiple databases enhanced for more flexible patent
number searching
NEWS 19 OCT 22 Current-awareness alert (SDI) setup and editing
enhanced
NEWS 20 OCT 22 WPIDS, WPINDEX, and WPIX enhanced with Canadian PCT
Applications
NEWS 21 OCT 24 CHEMLIST enhanced with intermediate list of
pre-registered REACH substances
NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,
AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.
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NEWS IPC8 For general information regarding STN implementation of IPC 8

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FILE 'HOME' ENTERED AT 07:49:41 ON 17 NOV 2008

=> file reg
COST IN U.S. DOLLARS

SINCE FILE TOTAL

FULL ESTIMATED COST

ENTRY SESSION
0.21 0.21

FILE 'REGISTRY' ENTERED AT 07:50:04 ON 17 NOV 2008
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DICTIONARY FILE UPDATES: 16 NOV 2008 HIGHEST RN 1072892-84-2

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=> S TGAAATGCTCAGATT/SQSN
L1 134 TGAAATGCTCAGATT/SQSN

=> S ATGAAATGCTCAGAT/SQSN
L2 142 ATGAAATGCTCAGAT/SQSN

=> S AATGAAATGCTCAGA/SQSN
L3 130 AATGAAATGCTCAGA/SQSN

=> S GAATGAAATGCTCAG/SQSN
L4 89 GAATGAAATGCTCAG/SQSN

=> S TGAATGAAATGCTCA/SQSN
L5 145 TGAATGAAATGCTCA/SQSN

=> s l1 or l2 or l3 or l4 or l5
L6 497 L1 OR L2 OR L3 OR L4 OR L5

=> s 197543-85-4/rn
L7 1 197543-85-4/RN

=> s l7 and l6
L8 1 L7 AND L6

=> d rn hit seq

L8 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2008 ACS on STN
RN 197543-85-4 REGISTRY

SEQ 1 acgatcngtn anatangga attgctccnc attncgtgta ntccantggt
51 tccactcaat ccttttagtc tggttctctg aggcagctga tgtcccat
101 catccagtgta tcattcagcc ttgtttactg cctgcatgtn gacttgtgcc
151 taaattgatt gatggcgta cctgcataa tgttgcncca gtttctgtgc
201 tattataaca acagccanta tgaaccagg cngcagttgt gtcggtgata

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251 tctaatacct ctgtgccnat gatgaccac attctttgtc cagcatatcc
301 tctgtnaatt accattttta cactgtgtgt aagcnggagc acaaaactaga
351 aagagtataa tcattgaaat gtcagattc ccatctgctt ctataatttg

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401 tgccatatcc aaacaancta ccttcattta aacggatttg ttcatgtgtt
451 tctacncgtt agtgcccacc atttgccatg caccttgnag agccncancc
501 cactgcnctg gttctctgca caaggttncc ctggccattg gcccnga

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HITS AT: 365-379

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SEQ      1 acgacngtn anagangga attgctcnc attncgtga nttcantgtt
51 tccactcaat ccttttagtc tggttctctg aggcagctga tgtccaccat
101 catccagtga tcattcagcc ttgtttactg cctgcatgtn gacttgtgcc
151 taaattgatt gatggcgta cctgcataa tgttgcncca gtttctgtgc
201 tattataaca acagccanta tgaaccagg cngcagttgt gtcgttgata
251 tctaatacct ctgtgccnat gatgaccac attctttgtc cagcatatcc
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351 aagagtataa tcattgaaat gtcagattc ccatctgctt ctataatttg

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401 tgccatatcc aaacaancta ccttcattta aacggatttg ttcatgtgtt
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HITS AT: 365-379

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